

DECLARATION Page 1 of 2 TEN XFW

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Nadejda G. Gurskaya, et al.

Serial No.: 10/501,629

Confirmation No.: 9951

Filed:

July 15, 2004

For: NOVEL FLUORESCENT

PROTEIN FROM AEQUOREA

COERULSCENS AND METHODS FOR USING THE

SAME

Group Art Unit: 1656

Examiner: Maryam Monshipouri

MAIL STOP AMENDMENT Commissioner for Patents P.O. Box 1450 Alexandria, VA 22313-1450 CERTIFICATE OF MAILING 37 CFR 1.8

I hereby certify that this correspondence is being deposited with sufficient postage as first class mail in an envelope addressed to: Mail Stop Amendment, Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450 on 3 /2 8 / 2008

Keith M. Tackett

Typed Name 32,008

Reg. No. if applicable

Signature

(713) 623-4844 Telephone Number

DECLARATION UNDER 37 C.F.R. §1.132

- I. Sergey Lukyanov, hereby declare and state that:
- 1. I am a scientist at <u>Shemyakin and Ovchinnikov Institute of Bioorganic Chemistry</u> (<u>Moscow, Russia</u>), <u>Evrogen JSC</u>, and I <u>am</u> one of the inventors of the subject application.
- I have worked in the molecular biology field for <u>22</u> years.
- 3. I have a Ph.D. degree in Molecular Biology from 1993 and a D.Sc. degree in Molecular Biology from 1999.
- 4. I declare that I have read the specification of United States Patent Application Serial No. 10/501,629 (the '629 application), filed July 15, 2004, the pending claims and the final Office Action dated January 23, 2008.

- 5. Paragraphs [00105] and [00106] of the '629 application describe a MegAlign algorithm used to determine "sequence identity."
- 6. The MegAlign clustal algorithm described in the '629 application is calculated by comparing two optimally aligned sequences, determining the number of positions at which the identical amino acid occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions, and multiplying the result by 100. The MegAlign algorithm accounts for all mismatches, without preference, regardless of whether or not the mismatch is a conserved mismatch.
- 7. As used in the '629 application, common understanding of the term "sequence identity" also requires comparing two optimally aligned sequences, determining the number of positions at which the identical amino acid occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions, and multiplying the result by 100.
- 8. Based on the description in the '629 application, the claim language "at least 96% identical" is understood to be determined by the following equation:

 (number of amino acid matches) / (total number of amino acids) * 100.
- 9. Attachments 3 and 4 of the final Office Action identify a "Query Match" term and a "Best Local Similarity" term. The "Query Match" term does not consider conservative mismatches equivalent to other mismatches. As an example, Attachment 3 identifies "Length 238" and "Matches 221" such that (number of amino acid matches) / (total number of amino acids) * 100 is:

221 / 238 * 100 = 92.9% (the same as the "Best Local Similarity").

10. Sequences shown in Attachments 3 and 4 of the final Office Action are respectively only 92.9% and 91.2% identical to SEQ ID NO: 2 referenced in claim 1 of the '629 application, and thereby are not "at least 96% identical to the Aequorea coerulescens non-fluorescent protein of SEQ ID NO: 2," as recited in claim 1.

The undersigned, <u>Sergey Lukyanov</u>, hereby declares that all statements made herein of my own knowledge are true and that these statements made on information and belief are believed to be true and further that these statements were made with knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of this application or any patent resulting therefrom.

Date: March 27, 2008

Signature



SEQUENCE LISTING

Fradkov, Arkadiy Lukyanov, Sergey Punkova, Natalia <120> Fluorescent Protein From Aequorea Coerulscens And Uses Thereof <130> EVRO-0006 <140> US 10/501,629 <141> 2005-07-15 <160> 25 <170> FastSEQ for Windows Version 4.0 <210> 1 <211> 941 <212> DNA <213> Aequoria coerulescens <400> 1 attcaaaaca ctgcagaatt ttggatagat tttcctgcta cttcacacgc ataaaagaca 60 agaaagatga gtaaaggagc agaacttttc actggagttg tcccaattct tattgaatta 120 aatggtgatg ttaatgggca caaattctct gtcagtggag agggcgaagg tgatgcgaca 180 tacggaaagt taacccttaa atttatttgc actacaggaa aactacctgt tccatggcca 240 acacttgtca ctactttctc ttatggtgtt caatgctttt caagatatcc agatcatatg 300 aaacagcatg acttetteaa gagtgeeatg eetgaaggtt atatacagga aagaactata 360 tttttcaaag atgacgggaa ctacaagtcg cgtgctgaag tcaagttcga aggtgatacc 420 ctggttaata gaattgagtt aacaggtact gattttaaag aagatggaaa catccttgga 480 aataaaatgg aatacaacta taacgcacat aatgtataca tcatgacaga caaagcaaaa 540 aatqqaatca aaqttaactt caaaattaqa cacaacattg aagatqqaag cqttcaactt 600 gcagaccatt atcaacaaaa tactccaatt ggcgatggcc ctgtcctttt accagataac 660 cattacctgt ccacacaatc taccetttee aaagateeca aegaaaagag agateacatg 720 atctattttg agtttgtaac agctgctgcg attacacatg gcatggatga attatacaaa 780 taaatgtata gacttcaagt tgacactaac gtgtccgaac aattactaaa atctcagggt 840 tcctggttaa aatcaggctg agatattatt tacatattat agattcatta gaattattta 900 aatactttat agatgttatt gataggggtt attttcttat t 941 <210> 2 <211> 238 <212> PRT <213> Aequoria coerulescens <400> 2 Met Ser Lys Gly Ala Glu Leu Phe Thr Gly Val Val Pro Ile Leu Ile 10 Glu Leu Asn Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 25 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys

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